ADDITIVE EFFECTS OF TWO GROWTH QTL ON CATTLE CHROMOSOME 14

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INTRODUCTION

DNA-marker technology has the potential to assist seed-stock beef producers with genetic improvement of traits that are difficult to measure, and to assist research workers in identifying chromosomal regions containing quantitative trait loci (QTL), and eventually genes, which control animal performance traits. A collaborative study was established in 1995 between AgResearch in New Zealand (NZ) and Adelaide University in Australia to search for DNA markers significantly linked to production, carcass and meat quality traits in beef cattle. The present paper reports on a sub-set of that data, namely evidence from microsatellite markers on chromosome (Chr) 14 of significant linkage to growth traits and hot carcass weight (HSCW) at a standard level of trim.

MATERIAL AND METHODS

Trial design. The trial design involved two of the more extreme *Bos taurus* dam breeds, Jersey (J) and Limousin (L), mated to JxL or LxJ first-cross sires to produce back-cross calves. A total of about 400 heifer and steer progeny were generated in each country, by three sires per country. Animals were slaughtered in NZ at 24-28 months of age, after a diet of mainly pasture (no concentrate feeding), and in Australia at 34-40 months of age following grazing and then at least six months of feedlotting. They were allocated to slaughter in NZ in balanced groups, whilst in Australia all animals of each cohort (sex-by-year groups) were slaughtered together. There were two calf crops in NZ (1996 and 1997 births), and three in Australia (1996-98 births). Phenotypes in the present study were live weights at approximately 250, 400 and 600 days of age (W250, W400, W600), early weight gain from 250 to 400 days (EG), late weight gain from 400 to 600 days (LG), and HSCW. Grazing conditions were such that EG was a slower gain in Australia than in NZ.

Marker analyses and data analyses. Sire-derived alleles were determined for a total of 253 informative microsatellite loci (an average of 185 loci per sire group) spread across the whole genome, except for the X and Y Chr. There were 9 informative markers recorded on Chr 14, spanning from 6.2 to 78.7 cM (Kappes *et al*., 1997). Phenotypes were pre-adjusted to account for known fixed effects, and residuals were stored after standardisation by dividing by the phenotypic standard deviation (σ_P). Residual correlations and principal components (PC) were also calculated, in view of the likely close relationships among a number of the traits. Linkage on Chr 14 with each standardised trait or PC was tested using Knott *et al*. (1996) interval-mapping regression procedures, with SAS (Version 6.12, Proc. GLM) and "QTL express" software (Sealey *et al*., 2001). When mapping QTL, a significantly linked marker

($P < 0.05$, genome-wide test) was required to have an F-test statistic > 10.0 (6 single sires tested separately) or > 3.6 (across all sires together), using the criteria of Lander and Kruglyak (1995). The hypothesis of two separate QTL for growth was also tested for Chr 14.

RESULTS AND DISCUSSION

Significant markers. Two significant DNA regions were identified on Chr 14 (Figure 1). The first QTL (QTL1) was between microsatellites *ILSTS011* and *ILSTS008*, situated from approximately 10 to 30 cM (Kappes *et al*., 1997). The second QTL (QTL2) was between markers *BM4513* and *BL1036* from approximately 60 to 80 cM. Four of the growth traits (W250, W600, EG and LG) and HSCW were significantly linked to QTL1 (Table 1).

Table 1. Effects of QTL1 and QTL2 on weights and gains (defined in the text) in units of phenotypic standard deviations (σ_P)[A]; signs represent effects of Limousin-derived minus Jersey-derived alleles

Sire[B]	W250	W400	W600	HSCW	EG	LG
QTL1						
394						
402				0.43±0.17		
417			0.47±0.20	0.59±0.20		
361	0.80±0.20	0.50±0.20	0.71±0.20	0.70±0.20	-0.69±0.15	0.40±0.16
368				0.40±0.20		
398						0.57±0.16
QTL2						
394						
402						
417		0.54±0.20	0.64±0.21	0.65±0.21		
361	0.54±0.20		0.43±0.20		-0.63±0.15	
368						
398						
NZ mean[A]	203.1	274.7	381.1	229.1	668.6	464.7
NZ σ_P [A]	23.8	26.6	32.7	21.8	88.0	69.0
Aust mean[A]	228.6	252.3	361.4	334.7	160.7	570.0
Aust σ_P [A]	27.5	26.6	31.2	36.5	92.9	88.8

[A] Only significant effects reported ($P<0.05$). Units for means and σ_P : weights, kg; gains, g/d.
[B] The first three sires were used in New Zealand (NZ); the second three in Australia (Aust).

The apparent effect for W400 was slightly smaller than for the other weights. EG was also significantly linked to QTL2 (Table 1). The two-QTL model (Sealey *et al*., 2001) confirmed significant markers for EG at about 10 cM ($P < 0.05$) and about 80 cM ($P < 0.001$).

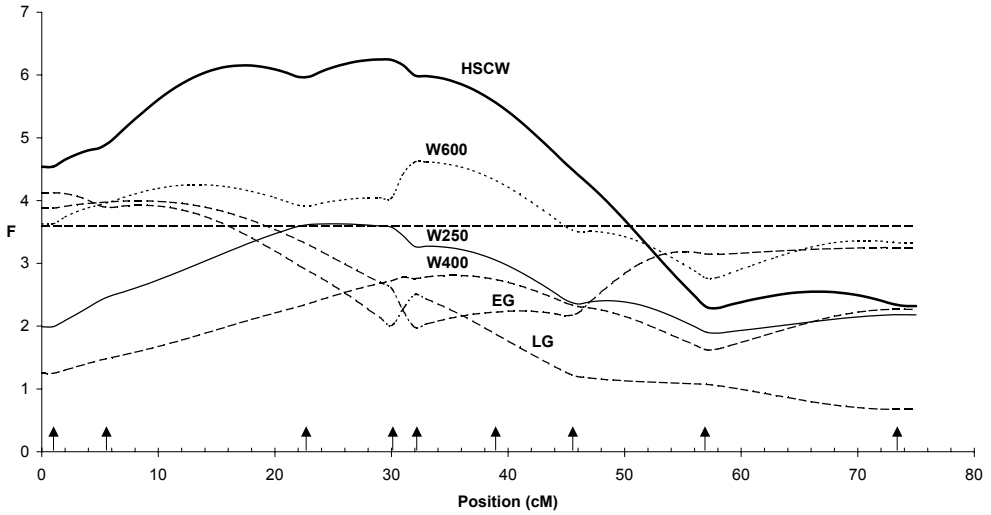

Figure 1. F-statistics for weights and gains (defined in the text) at 1 cM positions on chromosome 14; arrows indicate the positions of the microsatellites

Size of effects. The differences between the L-derived and J-derived alleles from the sire for QTL1 (at approximately 20 cM) or QTL2 (at approximately 70 cM) were significant as a t-test at $P < 0.05$ for many of the growth phenotypes in the progeny (Table 1). Live weights at various ages were highly correlated (range, 0.78 to 0.91), as also were live weights with HSCW (range, 0.62 to 0.79), so it was not surprising that a variety of growth phenotypes mapped to the same location. The PC analysis identified that the first PC accounted for 36% of the variance in 12 traits (weights and skeletal traits), and it also mirrored the likelihood curves for HSCW. Again, this was not surprising as the first PC represented body size. Interestingly, the J-derived allele increased EG, while the L-derived allele increased all the other growth measures shown and HSCW. Sire 361 in Australia (Table 1) had the most phenotypes significantly linked; σ_P for HSCW was 10.9% of the mean HSCW in Australia, so that the difference between this sire's QTL1 alleles corresponded to a 7.6% increase in HSCW. Allele effects in other weight traits ranged from 4 to 10% of their respective means.

Tests for QTL interactions. Various interactions with QTL1 were examined. There were no significant interactions of sex by QTL or of breed of dam by QTL. There were also no QTL1 by QTL2 interactions for EG.

Comparative mapping. Other authors have identified a QTL for linear traits or growth in cattle at similar positions on Chr 14. Spelman *et al*. (1999) reported a QTL for stature in cattle at 36 cM, closest to *BMS1941*. Buchanan *et al*. (2000) found a significant marker for growth in cattle at *BMS2934* (67 cM) and another in the centromeric region. Growth QTL in the same syntenic region have been also reported in pigs (Andersson *et al*., 1994; Wang *et al.,* 1998; Walling *et al*., 2000).

Candidate genes. There are many possible candidate genes in the general region of both QTL (http://www.gdb.org). One of the most promising for QTL1 is *myc*, a transcription factor known to activate growth promoting genes and repress growth arresting genes. Interestingly, the thyroglobulin gene (*TG*), which is associated with marbling in cattle (Barendse, 1997), also maps to the QTL1 region and the thyrotropin-releasing hormone receptor (*TRHR*) maps to the QTL2 region.

CONCLUSIONS

Our results showed that two QTL on Chr 14 were significantly linked to a series of growth traits including HSCW. There were additive effects between the two QTL for EG. In this case, although the markers could be used to assist with artificial selection, it may be less expensive to record the phenotype(s) instead, and then use index selection rather than marker-assisted selection. However, fine mapping around the marker sites may eventually lead to cloning of some of the underlying genes associated with growth, and hence may provide important insights into the biology of growth and its control.

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