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Preliminary beef carcass composition data from breed crosses in a genetic marker trial

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ABSTRACT

A collaborative project has been established in AgResearch and at the University of Adelaide to identify genetic markers for carcass composition and meat quality traits in beef cattle. Two extreme breeds were used, Jersey (J) and Limousin (L). First-cross Jersey x Limousin bulls (X) were mated to cows of both breeds to produce three-quarter Jersey (XJ) and three-quarter Limousin (XL) animals. A total of 261 and 155 back-cross cattle of both sexes were slaughtered as 2-year-olds at Ruakura in the springs of 1998 and 1999, respectively. A further 400 cattle of the same back-crosses are under evaluation in Australia. Relative to the mean off-pasture weight and hot carcass weight of the XJ cattle slaughtered at Ruakura in 1998 (404 and 202 kg), the corresponding XL means were 472 and 262 kg respectively, 1.8 and 2.6 phenotypic standard deviations (s.d.) heavier. A series of carcass composition traits was obtained from the weights of saleable meat, trimmed fat and bone from individual joints on the right side of each animal, after 24 h in the chiller. Over all joints, the weights of meat, fat and bone (as a % of their total) were 66.6, 9.6 and 23.8 for XJ and 71.7, 7.1 and 21.2 for XL, representing differences of 2.8, 1.4 and 2.2 s.d. units respectively. Weights of high value cuts (% of side weight) were 50.4 for XJ and 52.7 for XL, a 2.3 s.d. difference. Ratios of meat to bone were 2.80 for XJ and 3.93 for XL, a 5.5 s.d. difference. Standard errors of all the above differences in s.d. units were 0.16. The largest differences between the two breed crosses for the above traits were 2.8 and 5.5 s.d., for meat percent in the side, and for meat to bone ratio, providing good opportunities for genetic marker studies. In the AgResearch animals, consisting of progeny from three sire groups, markers from over half of the genome have been analysed so far. A significant marker has been identified for meat percent in the side. The two informative sires had the same genotype for this marker, and the difference between sire-derived alleles in their effect on meat percent averaged 0.99 s.d. (F statistic for each sire, 45.47 and 8.84).

Keywords: cattle; breeds; carcass composition; genetic marker.

INTRODUCTION

A genetic marker project was established in 1995 to search for quantitative trait loci (QTL) affecting beef meat quality and carcass composition. The project is a collaboration between AgResearch and the University of Adelaide. It uses a double back-cross design, in which first-cross bulls are mated to both parent breeds of cow, generating two types of three-quarterbred calves. The marker-search involves identifying those sire-derived alleles of the calves that are correlated with one or more performance measures ("phenotypes") on the same calves. The experiment is still in progress. The present report summarises the first year's carcass composition data in the two back-crosses at Ruakura, along with results showing at least one marker for differences in meat percent in the carcass side.

MATERIALS AND METHODS

Design

A double back-cross QTL design was established in 1995 using bulls which were first crosses between two *Bos taurus* breeds known to be widely different in a number of performance traits. The two breeds were Limousin (L) and Jersey (J), and they differed in carcass composition, fat colour, marbling, milk yield, body size, age at puberty, e.g., as reported by Cundiff *et al.* (1986). Back-cross cattle were generated in New Zealand and Australia. Three pairs of half-brothers were generated for mating as first crosses (X), and one of each pair was used in each country over both J and L cows. In New Zealand, 261 experimental back-cross

calves (162 XJ and 99 XL) were born in spring 1996, with another 155 born in spring 1997. The XJ calves were born on dairy farms and were bucket-reared; the XL calves were born following embryo transplant as singles or twins in 1996 to Hereford X Friesian recipients; in both years the XL calves were reared on their dams. Calves were slaughtered at approximately 2 years of age. In Australia, about 400 experimental back-cross calves were born over the 3 years 1996-98. This paper reports the comparisons of the 1996-born three-quarterbred cattle of both types ("breed groups") slaughtered at the Ruakura Experimental Abattoir in spring 1998.

Slaughter and dissection data

Animals in 1998 were pre-allocated to slaughter over 18 kill days (once per week x 15 animals per kill day, with 9 kill days each for heifers and steers). Pre-allocation was based on breed of sire, breed of dam and balanced as far as possible within calf breed for live weight before the first slaughter day. Hot carcass weight was recorded on the chain as the sum of the two side weights, and the right side was stored in a chiller for 24 hours before quartering at the 10/11th rib. A dissection of the two right quarters was then carried out using professional butchers, in order to record for each joint the weights of saleable meat plus meat trim (all referred to as "meat"), trimmed fat ("fat"), and bone.

Statistical analyses

Weights of components were totalled (for quarters, for high-value cuts or for the side) for meat, fat and bone, and percentages were calculated relative to their total. Meat to

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bone ratios were also calculated. Phenotypic standard deviations (s.d.) were obtained using SAS (1995), with a model consisting of sire of calf, slaughter group and breed group X birth rank interaction (n=3 classes, with one for XJ calves and two for XL calves (allowing for singles and twins), where the two XL classes were subsequently averaged). Differences between the two breed groups were expressed in s.d. units.

The sire-derived allele was determined for each calf, for at least 150 informative microsatellite marker loci spread across the whole genome, excluding the X and Y chromosomes. Linkage between each allele and carcass composition phenotypes was tested within sire on a genome-wide basis, using the multiple-marker regression approach of Knott *et al.* (1996), with fixed effects as described above. One marker linked to a carcass trait is discussed in detail, as an example.

RESULTS

Breed group differences

Table 1 shows the comparison of the two breed groups for off-pasture weight prior to slaughter, for hot carcass weight, and for carcass components. In s.d. units, the standard error of each trait is based on the same number of animals. Thus, the comparisons for all traits had the same standard error (0.16 s.d.), and all traits showed significant differences between breed groups ($P < 0.001$). These differences ranged from 1.4 to 5.5 s.d, and represented half of the additive difference between purebreds, although rearing differences and maternal effects could not be removed. The XL breed was, thus, heavier at fixed age, had heavier carcasses, higher dressing percent, relatively more meat, less fat, less bone, a higher ratio of meat to bone, and a higher percentage of high value cuts.

TABLE 1: Contrasts of two genetic groups (Jersey (XJ) and Limousin (XL)) for carcass composition traits

Trait	XJ	XL	Difference ¹
Off-pasture live weight, kg	404	472	1.8
Hot carcass weight, kg	202	262	2.6
Dressing percentage	50.0	55.3	3.7
% in the right side			
Meat	66.6	71.7	2.8
Trimmed fat	9.6	7.1	-1.4
Bone	23.8	21.2	-2.2
	100	100	
High-value cuts	50.4	52.7	2.3
Meat to bone ratio	2.80	3.93	5.5

¹ Difference, in standard deviation units, for XL minus XJ; standard errors were 0.16 standard deviation units (all $P < 0.001$).

Genetic marker search

As an example of the preliminary searches carried out for linkage between each informative marker and the carcass composition phenotypes, we describe here one significant marker (coded as marker MY) linked to the meat percent phenotype. Two sires used in the New Zealand part of the QTL study were heterozygous for this marker, and they had the same genotype. The difference between the sire-derived alleles in their effect on meat percent averaged 0.99

s.d. (F statistic for each sire, 45.47 and 8.84). The superior MY allele from each sire came from the L grandparent. Marker MY in these two sires explained one fifth of the difference in meat percent between the two back-crosses.

DISCUSSION

Breed group differences

For comparison with results in Table 1, Pitchford *et al.* (1998) reported figures for meat percent from 59 J, L x J and L steers (sons of the foundation parents in the QTL project), with means of 64.6, 66.6 and 73.6% respectively. The breed difference was 9.0%, and half of this (4.5%) was close to our estimate of 5.1%. Corresponding figures from Adelaide for side weight were 118, 158 and 186 kg, so that half the breed difference for hot carcass weight was expected to be 68 kg, similar to our value of 60 kg. Alternatively, relative to the J mean, the purebred L mean was 58% greater whereas, in our study, the difference of 30% above the J mean (half of the breed effect) was close to expectation.

Genetic markers

The marker MY described here as an example of significant linkage with a meat composition trait is important within this QTL data set, but not necessarily in others. Ideally fine mapping needs to be done to isolate the gene(s) responsible for the effect on meat percent, so that this region of the genome may be used more generally to increase meat percent in *Bos taurus* carcasses.

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